

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/720,363C
Source: P4/09
Date Processed by STIC: 7/11/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebs/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/720,363C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the ~~<220> "Feature"~~ and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

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use lower-case letters
for nucleotides

PCT

pg 1-3

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/09/720,363C

TIME: 15:04:05

Input Set : A:\Sequence Listing (to be submitted to PTO).txt

Output Set: N:\CRF4\07112005\I720363C.raw

1 <110> APPLICANT: Arima, Hidetoshi
3 Tsuchiya, Seishi
5 Hirata, Takahiro
7 Akiyama, Katsuhiko
9 Goto, Takashi
11 <120> TITLE OF INVENTION: Antisense Oligonucleotide Inhibiting IL-10 Protein
13 Expression
W--> 0 <130> FILE REFERENCE:
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/720,363C
17 <141> CURRENT FILING DATE: 2000-12-22
19 <150> PRIOR APPLICATION NUMBER: PCT/JP99/03315
W--> 21 <151> PRIOR FILING DATE: 1999-22-06 1999-06-22
23 <160> NUMBER OF SEQ ID NOS: 9

FYI: STC had problems
opening submitted disk.

Strong suggestion:
Consult

Does Not Comply
corrected Diskette Needed

ERRORED SEQUENCES

28 <210> SEQ ID NO: 1
30 <211> LENGTH: 18
32 <212> TYPE: DNA
C--> 34 <213> ORGANISM: ~~Nucleic Acid Artificial DNA~~
W--> 36 <220> FEATURE: ~~Feature of sequence~~ Corresponding to from +176 to +193 of
W--> 38 SEQ ID NO:9
40 <223> OTHER INFORMATION: ~~Antisense: YES, Single Strand, Topology: Straight~~
42 <400> SEQUENCE: 1
E--> 44 agaaagtctt cactctgc
46 <210> SEQ ID NO: 2
48 <211> LENGTH: 18
50 <212> TYPE: DNA
C--> 52 <213> ORGANISM: ~~Nucleic Acid Artificial DNA~~
W--> 54 <220> FEATURE: ~~Feature of sequence~~ Corresponding to from +181 to +198 of
W--> 55 SEQ ID NO:9
57 <223> OTHER INFORMATION: ~~Single-strand, Topology: Straight, Antisense: YES~~
59 <400> SEQUENCE: 2
E--> 61 ttgaaagaaa gtcttcac
64 <210> SEQ ID NO: 3
66 <211> LENGTH: 18
68 <212> TYPE: DNA
C--> 70 <213> ORGANISM: ~~Nucleic Acid Artificial DNA~~
W--> 72 <220> FEATURE: ~~Feature of sequence~~ Corresponding to from +367 to +384 of
W--> 74 SEQ ID NO:9
76 <223> OTHER INFORMATION: ~~Single-strand, Topology: Straight, Antisense: YES~~
78 <400> SEQUENCE: 3

invalid response - see item 10 on Error Summary
sheet goes on <2237> line

18 insert do not combine "old" sequence rules
cumulative format with "new"
base total sequence rules format
at right margin

1) NEVER
insert a
response
on <220>
line; it
is a
"header"
only.

2) give
source of
genetic
material
on
<2237> line

(see item 11 on Error
summary sheet) 7/11/05

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/720,363C

DATE: 07/11/2005

TIME: 15:04:05

Input Set : A:\Sequence Listing (to be submitted to PTO).txt

Output Set: N:\CRF4\07112005\I720363C.raw

E--> 80 ggtcttcagg ttctcccc 18 ←
 83 <210> SEQ ID NO: 4
 85 <211> LENGTH: 18
 87 <212> TYPE: DNA
 C--> 89 <213> ORGANISM: Nucleic Acid Artificial DNA
 W--> 91 <220> FEATURE: Feature of sequence: Corresponding to from +637 to +654 of
 W--> 93 SEQ ID NO:9
 95 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
 97 <400> SEQUENCE: 4
 E--> 99 ctgggtcagc tatcccag 18 ←
 102 <210> SEQ ID NO: 5
 104 <211> LENGTH: 18
 106 <212> TYPE: DNA
 C--> 108 <213> ORGANISM: Nucleic Acid Artificial DNA
 W--> 110 <220> FEATURE: Feature of sequence: Corresponding to from +915 to +932 of
 W--> 112 SEQ ID NO:9
 114 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
 116 <400> SEQUENCE: 5
 E--> 118 gcttggaatg gaagcttc 18 ←
 121 <210> SEQ ID NO: 6
 123 <211> LENGTH: 18
 125 <212> TYPE: DNA
 127 <213> ORGANISM: Nucleic Acid Synthesized DNA
 W--> 129 <220> FEATURE: Feature of Sequence: Corresponding to from +1246 to +1263
 W--> 131 of SEQ ID NO:9
 133 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
 135 <400> SEQUENCE: 6
 E--> 137 ggctggtag gaactcct 18 ←
 140 <210> SEQ ID NO: 7
 142 <211> LENGTH: 18
 144 <212> TYPE: DNA
 C--> 146 <213> ORGANISM: Nucleic Acid Artificial DNA
 W--> 148 <220> FEATURE: Feature of sequence: Corresponding to from +1249 to +1266 of
 W--> 150 SEQ ID NO:9
 152 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
 154 <400> SEQUENCE: 7
 E--> 156 ccaggctggt taggaact 18 ←
 159 <210> SEQ ID NO: 8
 161 <211> LENGTH: 18
 163 <212> TYPE: DNA
 C--> 165 <213> ORGANISM: Nucleic Acid Artificial DNA
 W--> 167 <220> FEATURE: Feature of sequence: Mouse IL-10 protein gene
 169 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
 171 <400> SEQUENCE: 8
 E--> 173 aggtcctgga gtccagca 18 ←

see P. 3

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3

<210>
<211>
<212>
<213>
<220>
<223>
<400>

9
1601
DNA

invabd <2137 response

cdna

Feature of sequence: cDNA of Human IL-10 protein

Single strand, Topology: Straight, Antisense: No

gone on <2237 line

9
aaaccacaag acagacttgc aaaagaaggc atgcacagct 40
cagcactgct ctgttgcttg gtcctcctga ctggggtgag 80
ggccagccca ggccaggga cccagtctga gaacagctgc 120
accacttcc caggcaacct gcctaactg cttcgagatc 160
tccgagatgc cttcagcaga gtgaagactt tctttcaaat 200
gaaggatcag ctggacaact tgttgtaaa ggagtccttg 240
ctggaggact ttaaggggta cctgggttgc caagccttgt 280
ctgagatgat ccagttttac ctggaggagg tgatgccccca 320
agctgagaac caagacccag acatcaaggc gcatgtgaac 360
tccctggggg agaacctgaa gacctcagg ctgaggctac 400
ggcgctgtca tctgatttctt ccctgtgaaa acaagagcaa 440
ggcgtggag caggtgaaga atgcctttaa taagctcca 480
gagaaaggca tctacaaagc catgagttag tttgacatct 520
tcatcaacta catagaagcc tacatgacaa tgaagatacg 560
aaactgagac atcagggtgg cgactctata gactctagga 600
cataaattag aggtctccaa aatcggatct ggggctctgg 640
gatagctgac ccagcccctt gagaaacctt attgtacctc 680
tcttatagaa tattttattac ctctgatacc tcaacccccca 720
tttctattta tttactgagc ttctctgtga acgatttaga 760
aagaagccca atattataat ttttttcaat atttattatt 800
ttcacctgtt tttaagctgt ttccataggg tgacacacta 840
tggtatttga gtgttttaag ataaattata agttacataa 880
gggaggaaaa aaaatgttct ttggggagcc aacagaagct 920
tccattccaa gcctgaccac gctttctagc tggtgagctg 960
ttttccctga cctccctcta atttatcttg tctctgggct 1000
tggggcttcc taactgctac aaatactctt aggaagagaa 1040
accaggggagc ccctttgatg attaattcac cttccagtgt 1080
ctcggaggga ttcccctaac ctcatcctcc aaccacttca 1120
ttcttgaaag ctgtggccag cttgttattt ataacaacct 1160
aaatttggtt ctaggccggg cgcggtggct cagcctgta 1200
atcccagcac tttgggaggc tgaggcgggt ggatcacttg 1240
aggtcaggag ttcctaacca gcctgggtcaa catgggtgaaa 1280
ccccgtctct actaaaaata caaaaattag ccgggcatgg 1320
tggcgcgcac ctgtaatccc agctacttgg gaggctgagg 1360
caagagaatt gcttgaaccc aggagatgga agttgcagtg 1400
agctgatatc atgcccctgt actccagcct gggtgacaga 1440
gcaagactct gtctcaaaaa aataaaaaata aaaataaatt 1480
tggttctaata agaactcagt tttaactaga atttattcaa 1520
ttcctctggg aatgttacat tgtttgtctg tcttcatagc 1560
agattttaat tttgaataaa taaatgtatc ttattcacat 1600
c 1601

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,363C

DATE: 07/11/2005

TIME: 15:04:06

Input Set : A:\Sequence Listing (to be submitted to PTO).txt

Output Set: N:\CRF4\07112005\I720363C.raw

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:21 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:34 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:36 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:38 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:44 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:1
L:44 M:112 C: (48) String data converted to lower case,
L:52 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:54 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:55 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:61 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:2
M:112 Repeated in SeqNo=2
L:70 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:72 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:74 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:3
M:112 Repeated in SeqNo=3
L:89 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:91 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:93 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:99 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:4
M:112 Repeated in SeqNo=4
L:108 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:110 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:112 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:118 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:5
M:112 Repeated in SeqNo=5
L:129 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:131 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:6
M:112 Repeated in SeqNo=6
L:146 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:148 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:150 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:156 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:7
M:112 Repeated in SeqNo=7
L:165 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:167 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:173 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:8
M:112 Repeated in SeqNo=8
L:184 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:190 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=9